Amendments to the Claims

This listing of claims replaces all prior versions and listings of claims in the application.

Listing of Claims:

1-6. (Cancelled)

7. (Currently amended) A method for identifying an agent that interacts with ER-β, the method comprising:

(a) providing a crystal structure of ER- β having a resolution of 1.83 Å or less;

(b) generating a three dimensional model of ER-β using the relative structural coordinates according to ~~Figure 2~~ FIGS. 2A-2XX, ± a root mean square deviation from the backbone atoms of the amino acids of not more than 1.5Å, the relative structural coordinates being based on the crystal structure of ER-β; and

(c) employing the three-dimensional model to design or select an agent that interacts with ER-β.

8. (Previously Presented) The method of claim 7, further comprising:

(d) obtaining the agent; and

(e) contacting the agent with ER-β in order to determine the effect the agent has on ER-β activity.

9. (Currently amended) A method for identifying an activator or inhibitor of ER-β, the method comprising:

(a) providing a crystal structure of ER-β having a resolution of 1.83 Å or less;

(b) generating a three dimensional model of ER-β using (i) the relative structural coordinates of amino acid residues MET343, LEU346, LEU349, GLU353, MET384, LEU387, MET388, ARG394, PHE404, ILE421, ILE424, GLY520, HIS523 and LEU524 according to

~~Figure 2~~ FIGS. 2A-2XX for monomer A of ER-β, ± a root mean square deviation from the backbone atoms of the amino acids of not more than 1.5Å, the relative structural coordinates of the amino acid residues for monomer A of ER-β being based on the crystal structure of ER-β or (ii) the relative structural coordinates of amino acid residues MET343, LEU346, LEU349, GLU353, MET384, LEU387, MET388, LEU391, ARG394, PHE404, ILE421, ILE424, GLY520, HIS523 and LEU524 according to ~~Figure 2~~ FIGS. 2A-2XX for monomer B of ER-β, ± a root mean square deviation from the backbone atoms of the amino acids of not more than 1.5Å, the relative structural coordinates of the amino acid residues for monomer B of ER-β being based on the crystal structure of ER-β; and

(c) selecting or designing a candidate activator or inhibitor by performing computer fitting analysis of the candidate activator or inhibitor with the three dimensional model generated in step (b).

10. (Currently amended) The method of claim 9, wherein the structural coordinates according to (i) further comprise the relative structural coordinates of amino acid residues VAL328, MET342, SER345, THR347, LYS348, LEU349, ALA350, ASP351, LEU354, MET357, TRP383, GLU385, VAL386, MET389, GLY390, LEU391, MET392, LEU402, ILE403, ALA405, LEU408, VAL418, GLU419, GLY420, LEU422, GLU423, PHE425, LEU428, ALA516, SER517, LYS519, MET521, GLU522, LEU525, ASN526, MET527, LYS528, VAL533, VAL535, TYR536 and LEU538 according to ~~Figure 2~~ FIGS. 2A-2XX for monomer A of ER-β, ± a root mean square deviation from the backbone atoms of the amino acids of not more than 1.5Å, the relative structural coordinates of the amino acid residues for monomer A of ER-β being based on the crystal structure of ER-β.

11. (Currently amended) The method of claim 9, wherein the relative structural coordinates according to (ii) further comprise the relative structural coordinates of amino acid residues MET342, SER345, THR347, LYS348, ALA350, ASP351, MET357, TRP383, GLU385, VAL386, LEU387, MET389, GLY390, MET392, LEU402, ILE403, ALA405,

LEU408, VAL418, GLU419, GLY420, LEU422, GLU423, PHE425, LEU428, ALA516, SER517, LYS519, MET521, GLU522, LEU525, ASN526, MET527, LYS528, VAL533, TYR536 and LEU538 according to ~~Figure 2~~ FIGS. 2A-2XX for monomer B of ER-β , ± a root mean square deviation from the backbone atoms of the amino acids of not more than 1.5Å, the relative structural coordinates of the amino acid residues for monomer B of ER-β being based on the crystal structure of ER-β.

12. (Previously presented) The method of claim 9, further comprising the steps of:

(d) obtaining the candidate activator or inhibitor; and

(e) contacting the candidate activator or inhibitor with the molecule or molecular complex and determining the effect the candidate activator or inhibitor has on the molecule or molecular complex.

13. (Original) The method of claim 12, wherein the candidate activator or inhibitor is contacted with the molecule or molecular complex in the presence of genistein to determine the effect the candidate activator or inhibitor has on binding of the molecule or molecular complex to genistein.

14-15. (Cancelled)

16. (Previously presented) The method of claim 7, wherein the crystal structure of ER-β has a resolution of 1.8 Å.

17. (Previously presented) The method of claim 9, wherein the crystal structure of ER-β has a resolution of 1.8 Å.